



OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/276,935C

DATE: 12/12/2002

TIME: 16:44:08

Errors on pp.
3-5

Input Set : A:\PU3474US 11-02 Seqlist.txt

Output Set: N:\CRF4\12122002\I276935C.raw

4 <110> APPLICANT: KLIOWER, Steven A.
 5 JONES, Stacey A.
 6 WILLSON, Timothy M.
 8 <120> TITLE OF INVENTION: AN ORPHAN NUCLEAR RECEPTOR
 11 <130> FILE REFERENCE: PU3474US2
 13 <140> CURRENT APPLICATION NUMBER: 09/276,935C
 C--> 14 <141> CURRENT FILING DATE: 2002-11-27
 16 <150> PRIOR APPLICATION NUMBER: 60/079,593
 17 <151> PRIOR FILING DATE: 1998-03-27
 19 <160> NUMBER OF SEQ ID NOS: 18
 21 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 20
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Artificial Sequence
 28 <220> FEATURE:
 29 <223> OTHER INFORMATION: Probe
 31 <400> SEQUENCE: 1
 32 ctgctgcgca tccaggacat 20
 34 <210> SEQ ID NO: 2
 35 <211> LENGTH: 45
 36 <212> TYPE: DNA
 37 <213> ORGANISM: Artificial Sequence
 39 <220> FEATURE:
 40 <223> OTHER INFORMATION: Probe
 42 <400> SEQUENCE: 2
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 45 <210> SEQ ID NO: 3
 46 <211> LENGTH: 34
 47 <212> TYPE: DNA
 48 <213> ORGANISM: Artificial Sequence
 50 <220> FEATURE:
 51 <223> OTHER INFORMATION: Probe
 53 <400> SEQUENCE: 3
 54 ggggtgtggg gatccacagc tacctgtgat gcgc 34
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 57 <211> LENGTH: 31
 58 <212> TYPE: DNA
 59 <213> ORGANISM: Artificial Sequence
 61 <220> FEATURE:
 62 <223> OTHER INFORMATION: Probe
 64 <400> SEQUENCE: 4
 65 gatcagacag ttcatgaagt tcatctagat c 31

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Input Set : A:\PU3474US 11-02 Seqlist.txt

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67 <210> SEQ ID NO: 5
68 <211> LENGTH: 29
69 <212> TYPE: DNA
70 <213> ORGANISM: Artificial Sequence
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73 <223> OTHER INFORMATION: Probe
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79 <211> LENGTH: 29
80 <212> TYPE: DNA
81 <213> ORGANISM: Artificial Sequence
83 <220> FEATURE:
84 <223> OTHER INFORMATION: Probe
86 <400> SEQUENCE: 6
87 gatcaatatg aactcaaagg aggtcagtg 29
89 <210> SEQ ID NO: 7
90 <211> LENGTH: 29
91 <212> TYPE: DNA
92 <213> ORGANISM: Artificial Sequence
94 <220> FEATURE:
95 <223> OTHER INFORMATION: Probe
97 <400> SEQUENCE: 7
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101 <211> LENGTH: 29
102 <212> TYPE: DNA
103 <213> ORGANISM: Artificial Sequence
105 <220> FEATURE:
106 <223> OTHER INFORMATION: Probe
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114 <213> ORGANISM: Artificial Sequence
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124 <212> TYPE: PRT
125 <213> ORGANISM: Artificial Sequence
127 <220> FEATURE:
128 <223> OTHER INFORMATION: Probe
130 <400> SEQUENCE: 10
131 Met Lys Lys Gly His His His His His Gly
132 1 5 10

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Input Set : A:\PU3474US 11-02 Seqlist.txt

Output Set: N:\CRF4\12122002\I276935C.raw

135 <210> SEQ ID NO: 11

136 <211> LENGTH: 316

137 <212> TYPE: PRT

138 <213> ORGANISM: Artificial Sequence

140 <220> FEATURE:

141 <223> OTHER INFORMATION: Protein

143 <400> SEQUENCE: 11

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145 1 5 10 15

146 Thr Gln Pro Leu Gly Val Gln Gly Leu Thr Glu Glu Gln Arg Met Met

147 20 25 30

148 Ile Arg Glu Leu Met Asp Ala Gln Met Lys Thr Phe Asp Thr Thr Phe

149 35 40 45

150 Ser His Phe Lys Asn Phe Arg Leu Pro Gly Val Leu Ser Ser Gly Cys

151 50 55 60

152 Glu Leu Pro Glu Ser Leu Gln Ala Pro Ser Arg Glu Glu Ala Ala Lys

153 65 70 75 80

154 Trp Ser Gln Val Arg Lys Asp Leu Cys Ser Leu Lys Val Ser Leu Gln

155 85 90 95

156 Leu Arg Gly Glu Asp Gly Ser Val Trp Asn Tyr Lys Pro Pro Ala Asp

157 100 105 110

158 Ser Gly Gly Lys Glu Ile Phe Ser Leu Leu Pro His Met Ala Asp Met

159 115 120 125

160 Ser Thr Tyr Met Phe Lys Gly Ile Ile Ser Phe Ala Lys Val Ile Ser

161 130 135 140

162 Tyr Phe Arg Asp Leu Pro Ile Glu Asp Gln Ile Ser Leu Leu Lys Gly

163 145 150 155 160

164 Ala Ala Phe Glu Leu Cys Gln Leu Arg Phe Asn Thr Val Phe Asn Ala

165 165 170 175

166 Glu Thr Gly Thr Trp Glu Cys Gly Arg Leu Ser Tyr Cys Leu Glu Asp

167 180 185 190

168 Thr Ala Gly Gly Phe Gln Gln Leu Leu Leu Glu Pro Met Leu Lys Phe

169 195 200 205

170 His Tyr Met Leu Lys Lys Leu Gln Leu His Glu Glu Tyr Val Leu

171 210 215 220

172 Met Gln Ala Ile Ser Leu Phe Ser Pro Asp Arg Pro Gly Val Leu Gln

173 225 230 235 240

174 His Arg Val Val Asp Gln Leu Gln Glu Gln Phe Ala Ile Thr Leu Lys

175 245 250 255

176 Ser Tyr Ile Glu Cys Asn Arg Pro Gln Pro Ala His Arg Phe Leu Phe

177 260 265 270

178 Leu Lys Ile Met Ala Met Leu Thr Glu Leu Arg Ser Ile Asn Ala Gln

179 275 280 285

180 His Thr Gln Arg Leu Leu Arg Ile Gln Asp Ile His Pro Phe Ala Thr

181 290 295 300

182 Pro Leu Met Gln Glu Leu Phe Gly Ile Thr Gly Ser

183 305 310 315

186 <210> SEQ ID NO: 12

187 <211> LENGTH: 242

*must explain genetic source -
See cover summary sheet item 11*

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Input Set : A:\PU3474US 11-02 Seqlist.txt

Output Set: N:\CRF4\12122002\I276935C.raw

188 <212> TYPE: PRT

189 <213> ORGANISM: Artificial Sequence

191 <220> FEATURE:

192 <223> OTHER INFORMATION: Protein

Some error

194 <400> SEQUENCE: 12

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196 1 5 10 15
197 Glu Ala Glu Leu Ala Val Glu Pro Lys Thr Glu Thr Tyr Val Glu Ala
198 20 25 30
199 Asn Met Gly Leu Asn Pro Ser Ser Pro Asn Asp Pro Val Thr Asn Ile
200 35 40 45
201 Cys Gln Ala Ala Asp Lys Gln Leu Phe Thr Leu Val Glu Trp Ala Lys
202 50 55 60
203 Arg Ile Pro His Phe Ser Glu Leu Pro Leu Asp Asp Gln Val Ile Leu
204 65 70 75 80
205 Leu Arg Ala Gly Trp Asn Glu Leu Leu Ile Ala Ser Phe Ser His Arg
206 85 90 95
207 Ser Ile Ala Val Lys Asp Gly Ile Leu Leu Ala Thr Gly Leu His Val
208 100 105 110
209 His Arg Asn Ser Ala His Ser Ala Gly Val Gly Ala Ile Phe Asp Arg
210 115 120 125
211 Val Leu Thr Glu Leu Val Ser Lys Met Arg Asp Met Gln Met Asp Lys
212 130 135 140
213 Thr Glu Leu Gly Cys Leu Arg Ala Ile Val Leu Phe Asn Pro Asp Ser
214 145 150 155 160
215 Lys Gly Leu Ser Asn Pro Ala Glu Val Glu Ala Leu Arg Glu Lys Val
216 165 170 175
217 Tyr Ala Ser Leu Glu Ala Tyr Cys Lys His Lys Tyr Pro Glu Gln Pro
218 180 185 190
219 Gly Arg Phe Ala Lys Leu Leu Leu Arg Leu Pro Ala Leu Arg Ser Ile
220 195 200 205
221 Gly Leu Lys Cys Leu Glu His Leu Phe Phe Phe Lys Leu Ile Gly Asp
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223 Thr Pro Ile Asp Thr Phe Leu Met Glu Met Leu Glu Ala Pro His Gln
224 225 230 235 240
225 Met Thr

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229 <210> SEQ ID NO: 13

230 <211> LENGTH: 2146

231 <212> TYPE: DNA

232 <213> ORGANISM: Artificial Sequence

234 <220> FEATURE:

235 <223> OTHER INFORMATION: Probe

237 <400> SEQUENCE: 13

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238 tgaaatatag gtgagagaca agattgtctc ataccggggg aaatcataac ctatgactag 60
239 gacgggaaga ggaagcactg cctttacttc agtgggaatc tgggcctcag cctgcaagcc 120
240 aagtgttcac agtgaagaaa gcaagagaat aagctaatac tctgtcctg aacaaggcag 180
241 cggctccttg ctaaaactac tcttgatcgc atcctttgca cgggattgtt caaagtggac 240
242 ccacggggag aagtcggagc aaagaactta ccaccaagca gtccaagagg ccagagaagca 300
243 aacctggagg tgagacccaa agaaagctgg aacctgctg actttgiaca ctgtgaggac 360

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RAW SEQUENCE LISTING

DATE: 12/12/2002

PATENT APPLICATION: US/09/276,935C

TIME: 16:44:08

Input Set : A:\PU3474US 11-02 Seqlist.txt

Output Set: N:\CRF4\12122002\I276935C.raw

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244 acagagtcctg ttccctggaaa gccacagtcg aacgcagatg aggaagtcgg aggtccccc 420
245 atctgcccgtg tatgtggggg caagggccact ggcatacact tcaatgtcat gacatgtgaa 480
246 ggatgcaagg gctttttcag gagggccatg aaagcgaag cccggctgag gtgccccttc 540
247 cgggaagggcg cctgcgagat caccgggaag acccgggagc agtgccaggc ctgcgccttg 600
248 cgcaagtgcc tggagagcgg catgaagaag gagatgatca tgtccgaagc ggccgtggag 660
249 gagaggcggg ccttgatcaa ggggaagaaa agtgaacgga cagggaactc gccactggga 720
250 gtgcaggggc tgacagagga gcagcggatg atgatcaggg agctgatgga cgcctcagatg 780
251 aaaaccccttg acaactacct ctcccatttc aagaatttcc ggctgccagg ggtgcttagc 840
252 agtggctgcg agtggccaga gtctctgcag gccccatcga gggaagaagc tgccaagtgg 900
253 agccaggctc ggaaagatct gtgctctttg aaggctcttc tgcagctgcg gggggaggat 960
254 ggcagtgtct ggaactacaa acccccagcc gacagtggcg ggaaagagat ctctccctg 1020
255 ctgcccacaa tggtgacat gtcaacctac atgttcaaa gcatcatcag ctttgccaaa 1080
256 gtcattctct acttcaggga ctggccatc gaggaacaga tctccctgct gaagggggcc 1140
257 gctttcgagc tgtgtcaact gagattcaac acagtgttca acgcgagac tggaacctgg 1200
258 gagtglggcc gctgttcta ctgcttgaa gacactgcag gtggttcca gcaacttcta 1260
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263 ctccgcagca tcaatgctca gcacaccag cggctgctgc gcatccagga cataccccc 1560
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265 gggtgacacc tccgagaggc agccagacc agagccctct gagccgccac tcccgggcca 1680
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267 cctgctatga cagctggcta gcattctca ggaaggacat gggtgcccc caccgccagt 1800
268 tcagtctgta gggagtgaag ccacagactc ttacgtggag agtgcactga cctgtaggtc 1860
269 aggaccatca gagaggcaag gttgcccttt ccttttaaaa ggcctgtgg tctggggaga 1920
270 aateccctcag atcccactaa agtgcacagg tgtggaagg accaagcac caaggatagg 1980
271 ccattctggg tctatgccc catacccaag ttgttctgt tctgagctt ttctattgct 2040
272 acctctaata gtctgtctc ccacttccc ctcttccc tctcttccg agctgcttg 2100
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275 <210> SEQ ID NO: 14

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277 <212> TYPE: PRT

278 <213> ORGANISM: Artificial Sequence

280 <220> FEATURE:

281 <223> OTHER INFORMATION: Protein *Same time*

283 <400> SEQUENCE: 14

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284 Leu Glu Val Arg Pro Lys Glu Ser Trp Asn His Ala Asp Phe Val His
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286 Cys Glu Asp Thr Glu Ser Val Pro Gly Lys Pro Ser Val Asn Ala Asp
287 20 25 30
288 Glu Glu Val Gly Gly Pro Gln Ile Cys Arg Val Cys Gly Asp Lys Ala
289 35 40 45
290 Thr Gly Tyr His Phe Asn Val Met Thr Cys Glu Gly Cys Lys Gly Phe
291 50 55 60
292 Phe Arg Arg Ala Met Lys Arg Asn Ala Arg Leu Arg Cys Pro Phe Arg
293 65 70 75 80
294 Lys Gly Ala Cys Glu Ile Thr Arg Lys Thr Arg Arg Gln Cys Gln Ala
295 85 90 95

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/276,935C

DATE: 12/12/2002

TIME: 16:44:09

Input Set : A:\PU3474US 11-02 Seqlist.txt

Output Set: N:\CRF4\12122002\I276935C.raw

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date

Raw Sequence Listing Error Summary

0182

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/276,935C

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length
Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
 (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ✓ Use of <220>
Sequence(s) 11, 12, 14 missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown."
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

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DEC 30 2002

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BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 07/276,135C
Source: CIPE
Date Processed by STIC: 12/12/02

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THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

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FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/efb/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202